



FIGURE 1

SEQ ID NO:51 GAC GGA ATT AAT TTC GCA ACA GGG AAT TTA CCT GGT TGC TCT TTC TCT ATC TTC CTT CTG
SEQ ID NO:52 D G I N F A T G N L P G C S F S I F L L

SEQ ID NO:51 GCT TTG TTC TCA TGC TTG CTT ACA CCC ACA GCC GGG CTG GAG TAC CGT AAT GCC TCC GGA
SEQ ID NO:52 A L F S C L L T P T A G L E Y R N A S G
SEQ ID NO:138 (page 5)

SEQ ID NO:51 CTC TAC ATG GTA ACT AAC GAC TGC AGT AAC GGT AGT ATC GTG TAT GAG GCC GGG GAT ATT
SEQ ID NO:52 L Y M V T N D C S N G S I V Y E A G D I
SEQ ID NO:138 (page 6)

SEQ ID NO:51 ATC CTC CAC TTA CCT GGC TGT GTC CCC TGC GTA CGC TCT GGC AAT ACA TCA AGA TGC TGG
SEQ ID NO:52 I L H L P G C V P C V R S G N T S R C W
SEQ ID NO:155
SEQ ID NO:174 (page 6)

SEQ ID NO:51 ATC CCT GTG AGC CCY ACC GTC GCC GTG AAG TCG CCC TGC GCC ACC GCC TCT CTC CGC
SEQ ID NO:52 I P V S P T V A G A wobble, no effect on translation
SEQ ID NO:174
SEQ ID NO:190 (page 7)

SEQ ID NO:51 ACG CAC GTG GAT ATG ATG GTG GGR GCG GCC ACC CTA TGC TCA GCT CTC TAC GTA GGA GAC
SEQ ID NO:52 T H V D M M V G A A T L C S A L Y V G D
wobble, no effect on translation

SEQ ID NO:51 CTT TGT GGA GCG CTA TTT CTT GTY GGG CAG GGG TTC TCA TGG AGA CAT CGC CAG CAT TGG
SEQ ID NO:52 L C G A L F L V G Q G F S W R H R Q H W
wobble, no effect on translation

SEQ ID NO:51 ACT GTC CAG GAC TGC AAC TGT TCC ATC
SEQ ID NO:52 T V Q D C N C S I

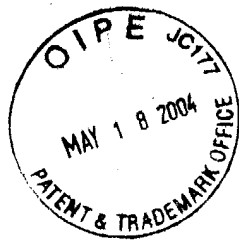


Figure 2 (page 1 of 2)
E1 nucleic acid

51	GACGGAATTA	ATTTGCAAC	AGGGAATTA	CCTGGTTGCT	CTTTCTCTAT	CTTCCCTTCTG
51	GCTTTGTTCT	CATGCTTGCT	TACACCCACA	GCCGGGCTGG	AGTACCGTAA	TGCCTCCGGA
HOTTA '046	CTCT	CATGCTTGCT	TACACCCACA	GCCGGGCTGG	AGTA	TCGTAA TGCCTCCGGA
51	CTCTACATGG	TAACTAACGA	CTGCAGTAAC	GGTAGTATCG	TGTATGAGGC	CGGGGATATT
51	CTCTACATAG	TAACTAACGA	CTGCAGTAAC	AGCAGTATCG	TGTATGAGGC	CCAGGATATT
51	ATCCTCCACT	TACCTGGCTG	TGTCCCCTGC	GTACGCTCTG	GCAATACATC	AAGATGCTGG
51	ATCCTCCACA	TGCTGGCTG	TGACCCCTGC	GTACGCTCTG	GCAACACATC	AAGCTGCTGG
51	ATCCCTGTGA	GCCYACCGT	CGCCGTGAAG	TCGCCCTGCG	CCGCCACCGC	CTCTCTCCGC
51	ACCCCTGTAA	GCCTACTGT	CGCTGTGGGT	CGCGCTGGCG	CTGCTACCGC	CTCTCTCCGC
51	ACGCACGTGG	ATATGATGGT	GGRGCGGCC	ACCCATATGCT	CAGCTCTCTA	CGTAGGAGAC
51	ACACATGTGG	ATATGATGGT	GGGAGCGGCC	ACCCCTTGCT	CAGCTCTCTA	CGTAGGAGAT
51	CTTTGTGGAG	CGCTATTCT	TGTYGGGCAG	GGGTTCTCAT	GGAGACATCG	CCAGCATTGG
51	CTTTGTGGAG	CGCTTTTCT	TGTTGGGCAG	GGGTTCTCAT	GGAGACATCG	CCAGCATTGG
51	ACTGTCCAGG	ACTGCAACTG	TTCCATC			
51	ACTGTCCAGG	ATTGCAACTG	TTCCATCTAC	CCTGGGCACC	TACACAGCCA	TCGTATG

Figure 2 (page 2 of 2)
E1 protein

52	DGINFATGNL	PGCSFSIFLL	ALFSCLLTPT	AGLEYRNASG	LYMVTNDCSN	GSIVYEAGDI
Hotta '046			LSCLLTPT	AGLEYRNASG	LYTNTNDCSN	SSIVYEAQDI
52	ILHLPGCVP	VRSGNTSRCW	IPVSPTVAVK	SPCAATASLR	THVDMMVGA	TLCsALYVGD
Hotta '046	ILHMPGCPC	VRSGNTSRCW	TPVSTTVAVG	RAGAAATASLR	THVDMMVGA	TLCsALYVGD
52	LCGALFLVGQ	GFSWRHRQHW	TVQDCNC	SIY		
Hotta '046	LCGALFLVGQ	GFSWRHRQHW	TVQDCNC	SIY	PGHLTGHRM	

